

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Olsen, Henrik S.  
Ruben, Steven M.
- (ii) TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Sterne, Kessler Goldstein & Fox P.L.L.C.
  - (B) STREET: 1100 New York Ave., NW, Suite 600
  - (C) CITY: Washington
  - (D) STATE: DC
  - (E) COUNTRY: USA
  - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: Patent Release #1.0, Version #1.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To be assigned
  - (B) FILING DATE: Herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/033,869
  - (B) FILING DATE: 20-DEC-1996
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/037,388
  - (B) FILING DATE: 07-FEB-1997
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Steffe, Eric K.
  - (B) REGISTRATION NUMBER: 36,688
  - (C) REFERENCE/DOCKET NUMBER: 1488.0440002
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 202-371-2600
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 860 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 20..505

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 20..79

(ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 80..505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCGCATACAG GCCCCACG ATG AAG GGT TTC ACA GCC ACT CTC TTC CTC TGG	52
Met Lys Gly Phe Thr Ala Thr Leu Phe Leu Trp	
-20 -15 -10	
ACT CTG ATT TTT CCC AGC TGC AGT GGA GGC GGC GGT GGG AAA GCC TGG	100
Thr Leu Ile Phe Pro Ser Cys Ser Gly Gly Gly Gly Lys Ala Trp	
-5 1 5	
CCC ACA CAC GTC GTC TGT AGC GAG AGC GGC PPG GAA GPG CTC TAC CAG	148
Pro Thr His Val Val Cys Ser Arg Ser Gly Leu Glu Val Leu Tyr Gln	
10 15 20	
AGT TGC GAT CCA TTA CAA GAT TTT GGC PTT TGT GTF GAA AAG TGT TCC	196
Ser Cys Asp Pro Leu Glu Asp Phe Gly Phe Ser Val Glu Lys Cys Ser	
25 30 35	
AAG CAA TTA AAA TCA AAT ATC AAC ATT AGA TTT GGA ATT ATT CTG AGA	244
Lys Glu Leu Ly Ser Asn Ile Asn Ile Arg Phe Gly Ile Ile Leu Arg	
40 45 50 55	
GAG GAC ATC AAA GAG CTT TTT CTT GAC CTA GCT CTC ATG TGT CAA GGC	292
Glu Asp Ile Lys Glu Leu Phe Leu Asp Leu Ala Leu Met Ser Gln Gly	
60 65 70	
TCA TTT GTT TTA AAT TTA TCC TAT CCC ATC PGT GAG GCG GCT CTG CCC	340
Ser Ser Val Leu Asn Phe Ser Tyr Pro Ile Cys Glu Ala Ala Leu Pro	
75 80 85	
AAG TTT TCT TTC TGT GGA AGA AGG AAA GGA GAG CAG ATT TAC TAT GCT	388
Lys Phe Ser Phe Cys Gly Arg Arg Lys Gly Glu Gln Ile Tyr Tyr Ala	
90 95 100	
GGG CCT GTC AAT AAT CTT GAA TTT ACT ATT CTT CAG GGA GAA TAC CAG	436
Gly Pro Val Asn Asn Pro Glu Phe Thr Ile Pro Gln Gly Glu Tyr Gln	
105 110 115	
GTT TTG CTG GAA CTG TAC ACT GAA AAA CGG TCC ACC GTG GCC TGT GCC	484
Val Leu Leu Glu Leu Tyr Thr Glu Lys Arg Ser Thr Val Ala Cys Ala	
120 125 130 135	
AAT GCT ACT ATC AAT TTT TCC TGACTGTGGC CTGTAGCAAA AATCACAGCC	532
Asn Ala Thr Ile Met Cys Ser	
140	
AGCTSCATCT CSTGGGACCT CCAAGCTCCT CTGACTGAAC CTACTGTGGG AGGAGAAGCA	596
GCTGATGACA GAGAGAGGCT CTACAAAGAA GCGCCCCCAA AGAGTGACAGC TGCTAATTTT	655
AGTCCCAGGA CCAGACATCC CCAGACTCCA CAGATGTAAT GAAGTCCCCG AATGTATCTG	715

TTTCTAAGGA GCGTCTTGGC AGTCCTTAAG CAGTCTTGAG GGTCCATCCT TTTTCTCTAA	775
TTGGTGGGCT CCCACCAGAC TCACGTGCTT TTCAACTTTT TAGGAGTGCT TCCTCACAGT	835
TACCAAGAAA TAAAGAAAGC TGGCC	860

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Gly	Phe	Thr	Ala	Thr	Leu	Phe	Leu	Trp	Thr	Leu	Ile	Phe	Pro	-20	-15	-10	-5
Ser	Cys	Ser	Gly	Gly	Gly	Gly	Gly	Lys	Ala	Trp	Pro	Thr	His	Val	Val	1	5	10	
Cys	Ser	Asp	Ser	Gly	Leu	Glu	Val	Leu	Tyr	Gln	Ser	Cys	Asp	Pro	Leu	15	20	25	
Gln	Asp	Phe	Gly	Phe	Ser	Val	Glu	Lys	Cys	Ser	Lys	Gln	Leu	Lys	Ser	30	35	40	
Asn	Ile	Asn	Ile	Arg	Phe	Gly	Ile	Ile	Leu	Arg	Glu	Asp	Ile	Lys	Glu	45	50	55	60
Leu	Phe	Leu	Asp	Leu	Ala	Leu	Met	Ser	Gln	Gly	Ser	Ser	Val	Leu	Asn	65	70	75	
Phe	Ser	Tyr	Pro	Ile	Cys	Glu	Ala	Ala	Leu	Pro	Lys	Phe	Ser	Phe	Cys	80	85	90	
Gly	Arg	Arg	Lys	Gly	Glu	Gln	Ile	Tyr	Tyr	Ala	Gly	Pro	Val	Asn	Asn	95	100	105	
Pro	Glu	Phe	Thr	Ile	Pro	Gln	Gly	Glu	Tyr	Gln	Val	Leu	Leu	Glu	Leu	110	115	120	
Tyr	Thr	Glu	Lys	Arg	Ser	Thr	Val	Ala	Cys	Ala	Asn	Ala	Thr	Ile	Met	125	130	135	140
Cys	Ser																		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STANDELNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Trp Pro Thr His Thr Val Cys Lys Glu Glu Asn Leu Glu Ile Tyr Tyr  
1 5 10 15  
Lys Ser Cys Asp Pro Gln Gln Asp Phe Ala Phe Ser Ile Asp Arg Cys  
20 25 30  
Ser Asp Val Thr Thr His Thr Phe Asp Ile Arg Ala Ala Met Val Leu  
35 40 45  
Arg Gln Ser Ile Lys Glu Leu Tyr Ala Lys Val Asp Leu Ile Ile Asn  
50 55 60  
Gly Lys Thr Val Leu Ser Tyr Ser Glu Thr Leu Cys Gly Pro Gly Leu  
65 70 75 80  
Ser Lys Leu Ile Phe Cys Gly Lys Lys Lys Gly Glu His Leu Tyr Tyr  
85 90 95  
Glu Gly Pro Ile Thr Leu Gly Ile Lys Glu Ile Pro Gln Gly Asp Tyr  
100 105 110  
Thr Ile Thr Ala Arg Leu Thr Asn Glu Asp Arg Ala Thr Val Ala Cys  
115 120 125  
Ala Asp Phe Thr Val  
130

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GACTCCATGG GCGGCGGTGG GAAAGCCTG

29

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACTAGATCT GGAGCACATG ATAGTAGCAT

30

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GACTGGATCC GCCATCATGA AGGGTTTCAC AGCCAC

36

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACTGGTACC ACCAGCTACA CTCTTTGGG

29

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGCTAAGCTT CCGCCACCAT GAAGGTTTC ACAGCC

36

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 62 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CASTCTCGAG	1TAAGCCTAG	2TCTGGGACGT	3CGTATGGGTA	4GGAGCACATG	5ATAGTAGCAT	60
7TG						62

(1) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GACTGGTACC	1AGCAGCTGCA	2CTCTTTGGG	3	29
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(1) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 514 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

NAATTGCGGA	1GATTCTTCCC	2AGCTCGAGTG	3GAGGCGGCGG	4TGGGAAAGCC	5TGGCCCCACAC	60
ACGTGGTCTG	7TAGCGACAGG	8CTTTGGAAGT	9GCTCTACCAG	10AGTTGCCGATC	11CATTACAAGA	120
TTTTGGCTTT	13TCTGTTGAAA	14AGTGTTCCAA	15GCAATTAAAA	16TCAAATATCA	17ACATTAGATT	180
TGGAAATTATT	19CTGAAGGACA	20TCAAAGAGCT	21TTTTCTTGAC	22CTAGCTCTCA	23TGTNTCAAGG	240
CTCATCTGTT	25TTGAATTTCT	26CCTATCCCAT	27CTGTGAGGCG	28GCTCTGCCAA	29GTTTTCTTTC	300
TGTGGAAGAA	32GGAAAGGAGA	33GCAGATTTAC	34TATGCTNGGG	35CTGTCAATAA	36TNCNGAATTT	360
ACTATTTGCT	39CANGGCCCAT	40TACCAGGTTT	41TGCTGGGACT	42GTACAATGAA	43AAACGGTCCA	420
CCGNBGNST	46GCCAIGCTAC	47TATCGNETGG	48TCCGACTGTG	49GCCNTAGGAA	50AATCACACCA	480
TTGNATTCGG	53GNCNCAGT	54CCTTCATNAC	55CNAN			514

(1) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 457 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACAGCCACT CTCTTCCTCT GGA	60
CTCTAAT TTNCCCAGC TGCAGTGGAG GCGGCGGTGG	
GAAAGCCTGG CCCACACACG TGGTCTGTAG CGACANGGCT TGAAGTGCT CTACCAGAGT	120
TGGATCCAT TACAAGATTT TGSETTTTCT GITGAAAAGT GTTCCAAGCA ATTA	180
AAAATCA TTAGATTTGG AATTATTCTG AGAGAGGACA TCAAAGAGCT TTTTCTTGAC	240
CTAGCTCTCA TGTCTCAAGG CTCATCTGTT TTNAATTTCT CCTATCCCAT CTGTNAGGGG	300
GCTCTGCCCA AGTTTTCTTT CTGTGGAAGA AGGAAAGGAG AGCAGATTTA CTATGCTGGG	360
CCTGTTCAAT AAATCCTGAA TTTAAGTATT CCTCAGGGAG AATACCAGGT TTTGCTGGAA	420
CTGTACACTG AAAAAAGGTC CAGGTGGGCG TGGGCA	480

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 413 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTGGTAACT GTGAGGAAGC ACTCTTAAAA AGTTGAAAAG CAGGTGAGTC TGGTGGGAGG	60
CGACCAATTA GAGAAAAAGG ATGGACCTC AAGACTGCTT AAGGACTGCC AAGAGGCTCC	120
TTAGAAACAG ATACATTGGG GGACTTCATT ACATCTGTGG AGTCTGGGA TGTCTGGTCC	180
TGGGACTAAA ATTAGCAGCT GCACTCTTTC GGGGCGCTTC TTTGTAGAGC CTCTCTCTGT	240
CATCAGCTGC TTCTCCTGCC ACAGTAGGTT CAGTCAGAGG AGCTTGGAGG TCCCACGAGA	300
TGCAGCTGGC TGTGATTTTT GCTACAGGCC ACAGTCAGGA GCACATGATA GTAGCATTGG	360
CACAGGCCAC GGTGGACCGT TTTTCAGTGT ACASTTCCAG CAAAACCTGG GTA	413

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 520 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGACATCAAA GAGCTTTTTC TTGACCTAGC ICTCATGTCT CAAGGCTCAT CTGTTTTGAA	60
TTTCTCCTAT CCCATCTGTG AGGCGGCTCT GCCAAGTTTT CTTTCTGTGG AAGAAGGAAA	120
GGAGAGCAGA TTTACTATGC TGGGCTGTG AATAATCCTG AATTTACTAT TCCTCAGGGA	180
GAATACCAGG TTTTGCTGGA ACTGTACACT GAAAAACGGT CCACCGTGGG CCTGTGNCAA	240
TGCTTACTAT TCATGTGCTC CTGACTGTGG GCCTGTTAGC AAAAANTCAC AGNCAGCTGC	300
ATCTCGTNGG GAACCTTCCA	320

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 264 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCAGAGGCC CACCATGAAG GGTTCACAG CCACTCTCTT CCTCTGGACT CTCATTTTTC	60
CCAGCTGCAG TGGAGGCGGC GGTGGGAAA GCCTGGCCCA CACAGGTGGT CTGTAGCGAC	120
AGNCTTTGGG AASTGCTCTA CCAGAGTTGG GATCCATTAC AAGATTTTGG CTTTCTGTTC	180
GAAAAGTGTT CCAAGCAATT AAAATCAAAT ATCAACATTA GATTGGANT TATTCTGAGA	240
GAGGACATCA AAGAGCTTTT TTTT	300

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 249 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCGATTAC AAGATNTTGG CTTNTCTGTT CAAAAGTGTT CCAAGCAATT AAAATCAAAT	60
ATCAACATTA GATTTGGAAT TATTCTGAGA GAGGACATCA AAGAGCTTTT TCTTGACCTA	120
GCTCTATGT CTCAGGCTC ATCTGTTTTG ANTTTCTCCT ATCCCATCTG TGAGGCGGCT	180
CTGCCAAGT TTTCTTTCTG TGNAGAAGG AAANGGGGNC AGNTTTACTT NTTCTTGTC	240
NTTTCNATT	249



(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Trp	Pro	Thr	His	Val	Cys	Leu	Glu	Tyr	Ser	Cys	Asp	Pro	Gln	Asp	Phe
1				5					10					15	
Phe	Ser	Cys	Ser	Ile	Arg	Leu	Arg	Ile	Lys	Glu	Leu	Leu	Gly	Val	Leu
			20					25					30		
Ser	Cys	Leu	Lys	Phe	Cys	Gly	Lys	Gly	Glu	Tyr	Tyr	Gly	Pro	Ile	Pro
		35					40					45			
Gln	Gly	Tyr	Leu	Glu	Arg	Thr	Val	Ala	Cys	Ala	Thr				
		50				55					60				